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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=6; day=24; hr=12; min=19; sec=54; ms=228;]

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Application No: 10593265 Version No: 2.0

Input Set:

Output Set:

Started: 2011-06-15 18:23:14.517
Finished: 2011-06-15 18:23:16.705
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 188 ms
Total Warnings: 24
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

Error code	Error Description
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Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> COMISSARIAT A L'ENERGIE ATOMIQUE
 RICHAUD, Pierre
 VERRET, Frederic
 GRAVOT, Antoine
 AUROY, Pascaline
 VAVASSEUR, Alain

<120> GENETICALLY MODIFIED PLANTS AND THEIR APPLICATIONS IN
 PHYTOREMEDIATION

<130> RICHAUD1

<140> 10593265

<141> 2011-06-15

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Met Ala Leu Gln Asn

1 5

aaa gaa gaa gag aaa aag aaa gtg aag aag ttg caa aag agt tac ttc 162

Lys Glu Glu Glu Lys Lys Lys Val Lys Lys Leu Gln Lys Ser Tyr Phe

10 15 20

gat gtt ctc gga atc tgt tgt aca tcg gaa gtt cct ata atc gag aat 210

Asp Val Leu Gly Ile Cys Cys Thr Ser Glu Val Pro Ile Ile Glu Asn

25 30 35

att ctc aag tca ctt gac ggc gtt aaa gaa tat tcc gtc atc gtt ccc 258

Ile Leu Lys Ser Leu Asp Gly Val Lys Glu Tyr Ser Val Ile Val Pro

40 45 50

tcg aga acc gtg att gtt gtt cac gac agt ctc ctc atc tct ccc ttc 306

Ser Arg Thr Val Ile Val Val His Asp Ser Leu Leu Ile Ser Pro Phe

55 60 65

caa att gct aag gca cta aac gaa gct agg tta gaa gca aac gtg agg 354

Gln Ile Ala Lys Ala Leu Asn Glu Ala Arg Leu Glu Ala Asn Val Arg

70 75 80 85

gta aac gga gaa act agc ttc aag aac aaa tgg ccg agc cct ttc gcc 402

Val Asn Gly Glu Thr Ser Phe Lys Asn Lys Trp Pro Ser Pro Phe Ala

90 95 100

gta gtt tcc ggc tta ctt ctc ctc cta tcc ttc cta aag ttt gtc tac 450

Val Val Ser Gly Leu Leu Leu Leu Leu Ser Phe Leu Lys Phe Val Tyr

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tcg cct tta cgt tgg ctc gcc gtg gca gca gtt gcc gcc ggt atc tat 498

Ser Pro Leu Arg Trp Leu Ala Val Ala Ala Val Ala Ala Gly Ile Tyr

120 125 130

ccg att ctt gcc aaa gcc ttt gct tcc att aaa agg cct agg atc gac 546

Pro Ile Leu Ala Lys Ala Phe Ala Ser Ile Lys Arg Pro Arg Ile Asp

135 140 145

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Trp Leu Glu Thr Arg Ala Ser Tyr Lys Ala Thr Ser Val Met Gln Ser	
185 190 195	
ctg atg agc tta gct cca caa aag gct ata ata gca gag act ggt gaa	738
Leu Met Ser Leu Ala Pro Gln Lys Ala Ile Ile Ala Glu Thr Gly Glu	
200 205 210	
gaa gtt gaa gta gat gag gtt aag gtt gat aca gtt gta gca gtt aaa	786
Glu Val Glu Val Asp Glu Val Lys Val Asp Thr Val Val Ala Val Lys	
215 220 225	
gct ggt gaa acc ata cca att gat gga att gtg gtg gat gga aac tgt	834
Ala Gly Glu Thr Ile Pro Ile Asp Gly Ile Val Val Asp Gly Asn Cys	
230 235 240 245	
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Glu Val Asp Glu Lys Thr Leu Thr Gly Glu Ala Phe Pro Val Pro Lys	
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cag aga gat tct acg gtt tgg gct ggc acc atc aat cta aat ggt tac	930
Gln Arg Asp Ser Thr Val Trp Ala Gly Thr Ile Asn Leu Asn Gly Tyr	
265 270 275	
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Ile Cys Val Lys Thr Thr Ser Leu Ala Gly Asp Cys Val Val Ala Lys	
280 285 290	
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Met Ala Lys Leu Val Glu Glu Ala Gln Ser Ser Lys Thr Lys Ser Gln	
295 300 305	
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Arg Leu Ile Asp Lys Cys Ser Gln Tyr Tyr Thr Pro Ala Ile Ile Leu	
310 315 320 325	
gta tca gct tgc gtt gcc att gtc ccg gtt ata atg aag gtc cac aac	1122
Val Ser Ala Cys Val Ala Ile Val Pro Val Ile Met Lys Val His Asn	
330 335 340	
ctt aaa cat tgg ttc cac cta gca tta gtt gtg tta gtc agt ggt tgt	1170
Leu Lys His Trp Phe His Leu Ala Leu Val Val Leu Val Ser Gly Cys	
345 350 355	
ccc tgt ggt ctt atc ctc tct aca cca gtt gct act ttc tgt gca ctt	1218
Pro Cys Gly Leu Ile Leu Ser Thr Pro Val Ala Thr Phe Cys Ala Leu	
360 365 370	
act aaa gcg gca act tca ggg ctt ctg atc aaa agt gct gat tat ctt	1266
Thr Lys Ala Ala Thr Ser Gly Leu Leu Ile Lys Ser Ala Asp Tyr Leu	
375 380 385	
gac aca ctc tca aag atc aag att gtt gct ttc gat aaa act ggg act	1314

Asp Thr Leu Ser Lys Ile Lys Ile Val Ala Phe Asp Lys Thr Gly Thr	
390 395 400 405	
att aca aga gga gag ttc att gtc ata gat ttc aag tca ctc tct aga	1362
Ile Thr Arg Gly Glu Phe Ile Val Ile Asp Phe Lys Ser Leu Ser Arg	
410 415 420	
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Asp Ile Asn Leu Arg Ser Leu Leu Tyr Trp Val Ser Ser Val Glu Ser	
425 430 435	
aaa tca agt cat cca atg gca gca aca atc gtg gat tat gca aaa tct	1458
Lys Ser Ser His Pro Met Ala Ala Thr Ile Val Asp Tyr Ala Lys Ser	
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Val Ser Val Glu Pro Arg Pro Glu Glu Val Glu Asp Tyr Gln Asn Phe	
455 460 465	
cca ggt gaa gga atc tac ggg aag att gat ggt aac gat atc ttc att	1554
Pro Gly Glu Gly Ile Tyr Gly Lys Ile Asp Gly Asn Asp Ile Phe Ile	
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Gly Asn Lys Lys Ile Ala Ser Arg Ala Gly Cys Ser Thr Val Pro Glu	
490 495 500	
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Ile Glu Val Asp Thr Lys Gly Gly Lys Thr Val Gly Tyr Val Tyr Val	
505 510 515	
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Gly Glu Arg Leu Ala Gly Phe Phe Asn Leu Ser Asp Ala Cys Arg Ser	
520 525 530	
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Gly Val Ser Gln Ala Met Ala Glu Leu Lys Ser Leu Gly Ile Lys Thr	
535 540 545	
gca atg cta acg gga gat aat caa gcc gcg gca atg cat gct caa gaa	1794
Ala Met Leu Thr Gly Asp Asn Gln Ala Ala Ala Met His Ala Gln Glu	
550 555 560 565	
cag cta ggg aat gtt tta gat gtt gta cat gga gat ctt ctt cca gaa	1842
Gln Leu Gly Asn Val Leu Asp Val Val His Gly Asp Leu Leu Pro Glu	
570 575 580	
gat aag tcc aga atc ata caa gag ttt aag aaa gag gga cca acc gca	1890
Asp Lys Ser Arg Ile Ile Gln Glu Phe Lys Lys Glu Gly Pro Thr Ala	
585 590 595	
atg gta ggg gac ggt gtg aat gat gca cca gct tta gct aca gct gat	1938
Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Thr Ala Asp	
600 605 610	
att ggt atc tcc atg gga att tct ggc tct gct ctt gca aca caa act	1986
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630	635	640	645
gtg aag cta gcg aga aga gca cga cgc aaa gtt gtt gaa aac gtg tgt			2082
Val Lys Leu Ala Arg Arg Ala Arg Arg Lys Val Val Glu Asn Val Cys			
	650	655	660
cta tcg atc att tta aaa gca gga ata ctc gct ttg gca ttt gct ggt			2130
Leu Ser Ile Ile Leu Lys Ala Gly Ile Leu Ala Leu Ala Phe Ala Gly			
	665	670	675
cat cct ttg att tgg gct gcg gtt ctt gtt gat gta ggg act tgt ctg			2178
His Pro Leu Ile Trp Ala Ala Val Leu Val Asp Val Gly Thr Cys Leu			
	680	685	690
ctt gtg att ttc aat agt atg ttg ctg ctg cga gag aag aaa aag att			2226
Leu Val Ile Phe Asn Ser Met Leu Leu Leu Arg Glu Lys Lys Lys Ile			
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ggg aac aaa aag tgt tac agg gct tct aca tct aag ttg aat ggt agg			2274
Gly Asn Lys Lys Cys Tyr Arg Ala Ser Thr Ser Lys Leu Asn Gly Arg			
710	715	720	725
aaa ctt gaa ggc gat gat gat tat gtt gtg gac tta gaa gca ggc ttg			2322
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	730	735	740
tta aca aag agc ggg aat ggt caa tgc aaa tca agc tgt tgt gga gat			2370
Leu Thr Lys Ser Gly Asn Gly Gln Cys Lys Ser Ser Cys Cys Gly Asp			
	745	750	755
aag aaa aat caa gag aac gtt gtg atg atg aaa cca agt agt aaa acc			2418
Lys Lys Asn Gln Glu Asn Val Val Met Met Lys Pro Ser Ser Lys Thr			
	760	765	770
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Ser Ser Asp His Ser His Pro Gly Cys Cys Gly Asp Lys Lys Glu Glu			
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aaa gtg aag ccg ctt gtg aaa gat ggc tgt tgc agt gag aaa act aag			2514
Lys Val Lys Pro Leu Val Lys Asp Gly Cys Cys Ser Glu Lys Thr Lys			
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aaa tca gag gga gat atg gtt tca ttg agc tca tgt aag aag tct agt			2562
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